

# Beã;ta G Vã©rtessy

## List of Publications by Year in descending order

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147  
papers

8,371  
citations

126708

33  
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49773

87  
g-index

157  
all docs

157  
docs citations

157  
times ranked

16984  
citing authors

#	ARTICLE	IF	CITATIONS
1	Primary Founder Mutations in the PRKDC Gene Increase Tumor Mutation Load in Colorectal Cancer. <i>International Journal of Molecular Sciences</i> , 2022, 23, 633.	1.8	2
2	Immobilization of the Aspartate Ammoniaâ€Lyase from <i>Pseudomonas fluorescens</i> R124 on Magnetic Nanoparticles: Characterization and Kinetics. <i>ChemBioChem</i> , 2022, 23, .	1.3	9
3	Assessment of Tractable Cysteines for Covalent Targeting by Screening Covalent Fragments. <i>ChemBioChem</i> , 2021, 22, 743-753.	1.3	19
4	Substrate Tunnel Engineering Aided by X-ray Crystallography and Functional Dynamics Swaps the Function of MIO-Enzymes. <i>ACS Catalysis</i> , 2021, 11, 4538-4549.	5.5	21
5	Detection of Genomic Uracil Patterns. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3902.	1.8	6
6	Viruses with U-DNA: New Avenues for Biotechnology. <i>Viruses</i> , 2021, 13, 875.	1.5	2
7	Whatâ€™s in a name? From â€fluctuation fitâ€to â€conformational selectionâ€ rediscovery of a concept. <i>History and Philosophy of the Life Sciences</i> , 2021, 43, 88.	0.6	2
8	Identification of new reference genes with stable expression patterns for gene expression studies using human cancer and normal cell lines. <i>Scientific Reports</i> , 2021, 11, 19459.	1.6	14
9	Identification of a nuclear localization signal in the Plasmodium falciparum CTP: phosphocholine cytidyltransferase enzyme. <i>Scientific Reports</i> , 2020, 10, 19739.	1.6	0
10	Structure-based inhibitor design of mutant RAS proteinsâ€”a paradigm shift. <i>Cancer and Metastasis Reviews</i> , 2020, 39, 1091-1105.	2.7	15
11	Rapid and quantitative antimalarial drug efficacy testing via the magneto-optical detection of hemozoin. <i>Scientific Reports</i> , 2020, 10, 14025.	1.6	11
12	Synthesis of New Chiral Crown Ethers Containing Phosphine or Secondary Phosphine Oxide Units. <i>Synthesis</i> , 2020, 52, 2870-2882.	1.2	3
13	Unshielding Multidrug Resistant Cancer through Selective Iron Depletion of P-Glycoproteinâ€Expressing Cells. <i>Cancer Research</i> , 2020, 80, 663-674.	0.4	21
14	Genome-wide alterations of uracil distribution patterns in human DNA upon chemotherapeutic treatments. <i>ELife</i> , 2020, 9, .	2.8	13
15	Beyond Chelation: EDTA Tightly Binds Taq DNA Polymerase, MutT and dUTPase and Directly Inhibits dNTPase Activity. <i>Biomolecules</i> , 2019, 9, 621.	1.8	6
16	Highly Sensitive and Rapid Characterization of the Development of Synchronized Blood Stage Malaria Parasites Via Magneto-Optical Hemozoin Quantification. <i>Biomolecules</i> , 2019, 9, 579.	1.8	12
17	HDX and Native Mass Spectrometry Reveals the Different Structural Basis for Interaction of the Staphylococcal Pathogenicity Island Repressor StI with Dimeric and Trimeric Phage dUTPases. <i>Biomolecules</i> , 2019, 9, 488.	1.8	7
18	Structural insights into the tyrosine phosphorylationâ€mediated inhibition of SH3 domainâ€ligand interactions. <i>Journal of Biological Chemistry</i> , 2019, 294, 4608-4620.	1.6	12

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19	The Role of a Key Amino Acid Position in Species-Specific Proteinaceous dUTPase Inhibition. <i>Biomolecules</i> , 2019, 9, 221.	1.8	3
20	Immobilized Whole-Cell Transaminase Biocatalysts for Continuous-Flow Kinetic Resolution of Amines. <i>Catalysts</i> , 2019, 9, 438.	1.6	33
21	Evaluation of critical design parameters for RTqPCR-based analysis of multiple dUTPase isoform genes in mice. <i>FEBS Open Bio</i> , 2019, 9, 1153-1170.	1.0	4
22	Mass spectrometry-based analysis of macromolecular complexes of <i>Staphylococcus aureus</i> uracil-DNA glycosylase and its inhibitor reveals specific variations due to naturally occurring mutations. <i>FEBS Open Bio</i> , 2019, 9, 420-427.	1.0	5
23	CRISPR/Cas9-Mediated Knock-Out of dUTPase in Mice Leads to Early Embryonic Lethality. <i>Biomolecules</i> , 2019, 9, 136.	1.8	13
24	An Acridone-Based Fluorescent Chemosensor for Cationic and Anionic Species, and Its Application for Molecular Logic Operations. <i>ChemistrySelect</i> , 2019, 4, 11936-11943.	0.7	6
25	The role of enzyme adsorption in the enzymatic degradation of an aliphatic polyester. <i>Enzyme and Microbial Technology</i> , 2019, 120, 110-116.	1.6	8
26	Search and destroy: versatile proteins offer unique structural solutions against uracil in DNA. <i>Amino Acids, Peptides and Proteins</i> , 2019, , 1-13.	0.7	0
27	The Stl repressor from <i>Staphylococcus aureus</i> is an efficient inhibitor of the eukaryotic fruitfly <i>scp</i> dUTPase. <i>FEBS Open Bio</i> , 2018, 8, 158-167.	1.0	7
28	Covalently immobilized Trp60Cys mutant of $\alpha$ -transaminase from <i>Chromobacterium violaceum</i> for kinetic resolution of racemic amines in batch and continuous-flow modes. <i>Biochemical Engineering Journal</i> , 2018, 132, 270-278.	1.8	29
29	Structural model of human dUTPase in complex with a novel proteinaceous inhibitor. <i>Scientific Reports</i> , 2018, 8, 4326.	1.6	15
30	Enzymatic degradation of poly-[(R)-3-hydroxybutyrate]: Mechanism, kinetics, consequences. <i>International Journal of Biological Macromolecules</i> , 2018, 112, 156-162.	3.6	22
31	Structural characterization of a sodium perchlorate-acridino-18-crown-6 ether complex. <i>Structural Chemistry</i> , 2018, 29, 113-118.	1.0	2
32	Uracil moieties in <i>Plasmodium falciparum</i> genomic <i>scp</i> DNA. <i>FEBS Open Bio</i> , 2018, 8, 1763-1772.	1.0	7
33	Exploiting a Phage-Bacterium Interaction System as a Molecular Switch to Decipher Macromolecular Interactions in the Living Cell. <i>Viruses</i> , 2018, 10, 168.	1.5	4
34	Heterologous expression of CTP:phosphocholine cytidyltransferase from <i>Plasmodium falciparum</i> rescues Chinese Hamster Ovary cells deficient in the Kennedy phosphatidylcholine biosynthesis pathway. <i>Scientific Reports</i> , 2018, 8, 8932.	1.6	2
35	Structural determinants of the catalytic mechanism of <i>Plasmodium</i> CCT, a key enzyme of malaria lipid biosynthesis. <i>Scientific Reports</i> , 2018, 8, 11215.	1.6	6
36	Perturbation of genome integrity to fight pathogenic microorganisms. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 3593-3612.	1.1	10

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37	The novel technique of vapor pressure analysis to monitor the enzymatic degradation of PHB by HPLC chromatography. <i>Analytical Biochemistry</i> , 2017, 521, 20-27.	1.1	5
38	Identification of Extracellular Segments by Mass Spectrometry Improves Topology Prediction of Transmembrane Proteins. <i>Scientific Reports</i> , 2017, 7, 42610.	1.6	15
39	A viral suppressor of RNA silencing inhibits ARGONAUTE 1 function by precluding target RNA binding to pre-assembled RISC. <i>Nucleic Acids Research</i> , 2017, 45, 7736-7750.	6.5	31
40	A Methylidene Group in the Phosphonic Acid Analogue of Phenylalanine Reverses the Enantioference of Binding to Phenylalanine Ammonia-lyases. <i>Advanced Synthesis and Catalysis</i> , 2017, 359, 2109-2120.	2.1	9
41	The First Enantioselective Total Synthesis of (âˆ“) - <i>trans</i> -Dihydronarciclasine. <i>Journal of Natural Products</i> , 2017, 80, 1909-1917.	1.5	18
42	Elevated APOBEC3B expression drives a kataegic-like mutation signature and replication stress-related therapeutic vulnerabilities in p53-defective cells. <i>British Journal of Cancer</i> , 2017, 117, 113-123.	2.9	84
43	Differential control of dNTP biosynthesis and genome integrity maintenance by the dUTPase superfamily enzymes. <i>Scientific Reports</i> , 2017, 7, 6043.	1.6	18
44	p53 controls expression of the DNA deaminase APOBEC3B to limit its potential mutagenic activity in cancer cells. <i>Nucleic Acids Research</i> , 2017, 45, 11056-11069.	6.5	70
45	Structural characterization of the crystalline diastereomeric complexes of enantiopure dimethylacridino-18-crown-6 ether and the enantiomers of 1-(1-naphthyl)ethylamine hydrogen perchlorate. <i>Structural Chemistry</i> , 2017, 28, 289-296.	1.0	3
46	Functional Analysis on a Naturally Occurring Variant of the Staphylococcus Aureus Uracil DNA Glycosylase Inhibitor. <i>Periodica Polytechnica: Chemical Engineering</i> , 2017, , .	0.5	1
47	A novel phenylalanine ammonia-lyase from <i>Kangiella koreensis</i> . <i>Studia Universitatis Babeş-Bolyai Chemia</i> , 2017, 62, 293-308.	0.1	7
48	Life without dUTPase. <i>Frontiers in Microbiology</i> , 2016, 7, 1768.	1.5	24
49	Secondary Structure Prediction of Protein Constructs Using Random Incremental Truncation and Vacuum-Ultraviolet CD Spectroscopy. <i>PLoS ONE</i> , 2016, 11, e0156238.	1.1	5
50	A Hidden Active Site in the Potential Drug Target Mycobacterium tuberculosis dUTPase Is Accessible through Small Amplitude Protein Conformational Changes. <i>Journal of Biological Chemistry</i> , 2016, 291, 26320-26331.	1.6	8
51	The nucleotidohydrolases DCTPP1 and dUTPase are involved in the cellular response to decitabine. <i>Biochemical Journal</i> , 2016, 473, 2635-2643.	1.7	17
52	Potential steps in the evolution of a fused trimeric all- $\beta$ dUTPase involve a catalytically competent fused dimeric intermediate. <i>FEBS Journal</i> , 2016, 283, 3268-3286.	2.2	5
53	Structural Characterization of Arginine Fingers: Identification of an Arginine Finger for the Pyrophosphatase dUTPases. <i>Journal of the American Chemical Society</i> , 2016, 138, 15035-15045.	6.6	32
54	Trading in cooperativity for specificity to maintain uracil-free DNA. <i>Scientific Reports</i> , 2016, 6, 24219.	1.6	8

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55	Detection of uracil within DNA using a sensitive labeling method for <i>in vitro</i> and cellular applications. <i>Nucleic Acids Research</i> , 2016, 44, e28-e28.	6.5	29
56	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). <i>Autophagy</i> , 2016, 12, 1-222.	4.3	4,701
57	Structural Biology and Regulation of Protein Import into the Nucleus. <i>Journal of Molecular Biology</i> , 2016, 428, 2060-2090.	2.0	204
58	In Vitro Analysis of Predicted DNA-Binding Sites for the Stl Repressor of the <i>Staphylococcus aureus</i> SaPIBov1 Pathogenicity Island. <i>PLoS ONE</i> , 2016, 11, e0158793.	1.1	9
59	Phenylalanine Ammonia-lyase-Catalyzed Deamination of an Acyclic Amino Acid: Enzyme Mechanistic Studies Aided by a Novel Microreactor Filled with Magnetic Nanoparticles. <i>ChemBioChem</i> , 2015, 16, 2283-2288.	1.3	46
60	Evidence-Based Structural Model of the Staphylococcal Repressor Protein: Separation of Functions into Different Domains. <i>PLoS ONE</i> , 2015, 10, e0139086.	1.1	16
61	Mutations Decouple Proton Transfer from Phosphate Cleavage in the dUTPase Catalytic Reaction. <i>ACS Catalysis</i> , 2015, 5, 3225-3237.	5.5	28
62	Structural characterization of a complex derived from lead(II) perchlorate and acridono-18-crown-6 ether. <i>Structural Chemistry</i> , 2015, 26, 1467-1471.	1.0	5
63	Immobilization of Phenylalanine Ammonia-lyase on Single-Walled Carbon Nanotubes for Stereoselective Biotransformations in Batch and Continuous-Flow Modes. <i>ChemCatChem</i> , 2015, 7, 1122-1128.	1.8	43
64	Cross-species inhibition of dUTPase via the Staphylococcal Stl protein perturbs dNTP pool and colony formation in <i>Mycobacterium</i> . <i>DNA Repair</i> , 2015, 30, 21-27.	1.3	20
65	dUTPase expression correlates with cell division potential in <i>Drosophila melanogaster</i> . <i>FEBS Journal</i> , 2015, 282, 1998-2013.	2.2	3
66	Exploring the role of the phage-specific insert of bacteriophage $\phi$ 11 dUTPase. <i>Structural Chemistry</i> , 2015, 26, 1425-1432.	1.0	5
67	Molecular Mechanism for the Thermo-Sensitive Phenotype of CHO-MT58 Cell Line Harboring a Mutant CTP:Phosphocholine Cytidyltransferase. <i>PLoS ONE</i> , 2015, 10, e0129632.	1.1	10
68	The Metagenomic Telescope. <i>PLoS ONE</i> , 2014, 9, e101605.	1.1	5
69	Dynamics of re-constitution of the human nuclear proteome after cell division is regulated by NLS-adjacent phosphorylation. <i>Cell Cycle</i> , 2014, 13, 3551-3564.	1.3	23
70	Highly potent dUTPase inhibition by a bacterial repressor protein reveals a novel mechanism for gene expression control. <i>Nucleic Acids Research</i> , 2014, 42, 11912-11920.	6.5	36
71	Preventive DNA repair by sanitizing the cellular (deoxy)nucleoside triphosphate pool. <i>FEBS Journal</i> , 2014, 281, 4207-4223.	2.2	38
72	NLS copy number variation governs efficiency of nuclear import – case study on dUTPases. <i>FEBS Journal</i> , 2014, 281, 5463-5478.	2.2	6

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73	Factors influencing nucleo-cytoplasmic trafficking: which matter? Response to Alvisi & Jans' comment on Phosphorylation adjacent to the nuclear localization signal of human dUTPase abolishes nuclear import: structural and mechanistic insights. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2777-2778.	2.5	0
74	Bisepoxide Cross-Linked Enzyme Aggregates—New Immobilized Biocatalysts for Selective Biotransformations. <i>ChemCatChem</i> , 2014, 6, 1463-1469.	1.8	14
75	Composite Aromatic Boxes for Enzymatic Transformations of Quaternary Ammonium Substrates. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 13471-13476.	7.2	20
76	Expression and Properties of the Highly Alkalophilic Phenylalanine Ammonia-Lyase of Thermophilic <i>Rubrobacter xylanophilus</i> . <i>PLoS ONE</i> , 2014, 9, e85943.	1.1	24
77	Investigations of homologous disaccharides by elastic incoherent neutron scattering and wavelet multiresolution analysis. <i>Chemical Physics</i> , 2013, 424, 56-61.	0.9	20
78	Evolutionary and mechanistic insights into substrate and product accommodation of CTP-phosphocholine cytidyltransferase from <i>Lasmodium falciparum</i> . <i>FEBS Journal</i> , 2013, 280, 3132-3148.	2.2	16
79	Expanding the DNA alphabet in the fruit fly. <i>Fly</i> , 2013, 7, 23-27.	0.9	10
80	Phosphorylation adjacent to the nuclear localization signal of human dUTPase abolishes nuclear import: structural and mechanistic insights. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2495-2505.	2.5	42
81	Structure and enzymatic mechanism of a moonlighting dUTPase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2298-2308.	2.5	21
82	Silicon carbide quantum dots for bioimaging. <i>Journal of Materials Research</i> , 2013, 28, 205-209.	1.2	40
83	Catalytic mechanism of $\gamma$ -phosphate attack in dUTPase is revealed by X-ray crystallographic snapshots of distinct intermediates, $^{31}\text{P}$ -NMR spectroscopy and reaction path modelling. <i>Nucleic Acids Research</i> , 2013, 41, 10542-10555.	6.5	14
84	Molecular cloning and characterization of a thermostable esterase/lipase produced by a novel <i>Anoxybacillus flavithermus</i> strain. <i>Journal of General and Applied Microbiology</i> , 2013, 59, 119-134.	0.4	14
85	Molecular Mechanisms of Survival Strategies in Extreme Conditions. <i>Life</i> , 2012, 2, 364-376.	1.1	13
86	Uracil-Containing DNA in <i>Drosophila</i> : Stability, Stage-Specific Accumulation, and Developmental Involvement. <i>PLoS Genetics</i> , 2012, 8, e1002738.	1.5	63
87	Enhanced Cellular Uptake of a New, in Silico Identified Antitubercular Candidate by Peptide Conjugation. <i>Bioconjugate Chemistry</i> , 2012, 23, 900-907.	1.8	31
88	The dUTPase Enzyme Is Essential in <i>Mycobacterium smegmatis</i> . <i>PLoS ONE</i> , 2012, 7, e37461.	1.1	44
89	Shared developmental roles and transcriptional control of autophagy and apoptosis in <i>Caenorhabditis elegans</i> . <i>Journal of Cell Science</i> , 2011, 124, 1510-1518.	1.2	34
90	Association of RNA with the uracil-DNA-degrading factor has major conformational effects and is potentially involved in protein folding. <i>FEBS Journal</i> , 2011, 278, 295-315.	2.2	6

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91	Cellular Response to Efficient dUTPase RNAi Silencing in Stable HeLa Cell Lines Perturbs Expression Levels of Genes Involved in Thymidylate Metabolism. <i>Nucleosides, Nucleotides and Nucleic Acids</i> , 2011, 30, 369-390.	0.4	21
92	Crystallization and preliminary crystallographic analysis of dUTPase from the $\phi$ 11 helper phage of <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1411-1413.	0.7	4
93	From $\alpha$ -fluctuation fit to $\alpha$ -conformational selection: Evolution, rediscovery, and integration of a concept. <i>BioEssays</i> , 2011, 33, 30-34.	1.2	31
94	Nucleotide pyrophosphatase employs a P-loop-like motif to enhance catalytic power and NDP/NTP discrimination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 14437-14442.	3.3	30
95	Proteins with Complex Architecture as Potential Targets for Drug Design: A Case Study of <i>Mycobacterium tuberculosis</i> . <i>PLoS Computational Biology</i> , 2011, 7, e1002118.	1.5	21
96	Calpain-Catalyzed Proteolysis of Human dUTPase Specifically Removes the Nuclear Localization Signal Peptide. <i>PLoS ONE</i> , 2011, 6, e19546.	1.1	8
97	Discovery of Novel MDR- <i>Mycobacterium tuberculosis</i> Inhibitor by New FRIGATE Computational Screen. <i>PLoS ONE</i> , 2011, 6, e28428.	1.1	13
98	Study of solvent-protein coupling effects by neutron scattering. <i>Journal of Biological Physics</i> , 2010, 36, 207-220.	0.7	16
99	Direct contacts between conserved motifs of different subunits provide major contribution to active site organization in human and mycobacterial dUTPases. <i>FEBS Letters</i> , 2010, 584, 3047-3054.	1.3	17
100	Physiological truncation and domain organization of a novel uracil-DNA-degrading factor. <i>FEBS Journal</i> , 2010, 277, 1245-1259.	2.2	5
101	<i>Drosophila</i> proteins involved in metabolism of uracil-DNA possess different types of nuclear localization signals. <i>FEBS Journal</i> , 2010, 277, 2142-2156.	2.2	9
102	Aromatic stacking between nucleobase and enzyme promotes phosphate ester hydrolysis in dUTPase. <i>Nucleic Acids Research</i> , 2010, 38, 7179-7186.	6.5	80
103	A one-step method for quantitative determination of uracil in DNA by real-time PCR. <i>Nucleic Acids Research</i> , 2010, 38, e196-e196.	6.5	35
104	Structure and mechanism of calmodulin binding to a signaling sphingolipid reveal new aspects of lipid-protein interactions. <i>FASEB Journal</i> , 2010, 24, 3829-3839.	0.2	8
105	Dissociation of Calmodulin-Target Peptide Complexes by the Lipid Mediator Sphingosylphosphorylcholine. <i>Journal of Biological Chemistry</i> , 2010, 285, 1799-1808.	1.6	18
106	Molecular shape and prominent role of $\beta$ -strand swapping in organization of dUTPase oligomers. <i>FEBS Letters</i> , 2009, 583, 865-871.	1.3	23
107	Improving thermostability and catalytic activity of pyranose 2-oxidase from <i>Trametes multicolor</i> by rational and semi-rational design. <i>FEBS Journal</i> , 2009, 276, 776-792.	2.2	37
108	Keeping Uracil Out of DNA: Physiological Role, Structure and Catalytic Mechanism of dUTPases. <i>Accounts of Chemical Research</i> , 2009, 42, 97-106.	7.6	213

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109	Nuclear localization signal-dependent and -independent movements of <i>Drosophila melanogaster</i> dUTPase isoforms during nuclear cleavage. <i>Biochemical and Biophysical Research Communications</i> , 2009, 381, 271-275.	1.0	13
110	Methylene substitution at the Î±-Î² bridging position within the phosphate chain of dUDP profoundly perturbs ligand accommodation into the dUTPase active site. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 308-319.	1.5	31
111	Neutron scattering studies on dUTPase complex in the presence of bioprotectant systems. <i>Chemical Physics</i> , 2008, 345, 250-258.	0.9	28
112	Active site of mycobacterial dUTPase: Structural characteristics and a built-in sensor. <i>Biochemical and Biophysical Research Communications</i> , 2008, 373, 8-13.	1.0	60
113	Kinetic Mechanism of Human dUTPase, an Essential Nucleotide Pyrophosphatase Enzyme. <i>Journal of Biological Chemistry</i> , 2007, 282, 33572-33582.	1.6	58
114	A novel fruitfly protein under developmental control degrades uracil-DNA. <i>Biochemical and Biophysical Research Communications</i> , 2007, 355, 643-648.	1.0	22
115	Active site closure facilitates juxtaposition of reactant atoms for initiation of catalysis by human dUTPase. <i>FEBS Letters</i> , 2007, 581, 4783-4788.	1.3	58
116	Quantitative determination of uracil residues in <i>Escherichia coli</i> DNA: Contribution of ung, dug, and dut genes to uracil avoidance. <i>DNA Repair</i> , 2006, 5, 1407-1420.	1.3	52
117	Crystallization and preliminary X-ray studies of dUTPase from Mason-Pfizer monkey retrovirus. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 399-401.	0.7	7
118	Flexible segments modulate co-folding of dUTPase and nucleocapsid proteins. <i>Nucleic Acids Research</i> , 2006, 35, 495-505.	6.5	42
119	Developmental Regulation of dUTPase in <i>Drosophila melanogaster</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 22362-22370.	1.6	38
120	Altered Active Site Flexibility and a Structural Metal-binding Site in Eukaryotic dUTPase. <i>Journal of Biological Chemistry</i> , 2004, 279, 17932-17944.	1.6	42
121	Structural Insights into the Catalytic Mechanism of Phosphate Ester Hydrolysis by dUTPase. <i>Journal of Biological Chemistry</i> , 2004, 279, 42907-42915.	1.6	75
122	Multidimensional NMR Identifies the Conformational Shift Essential for Catalytic Competence in the 60-kDa <i>Drosophila melanogaster</i> dUTPase Trimer. <i>Journal of Biological Chemistry</i> , 2004, 279, 17945-17950.	1.6	13
123	A tradeoff between protein stability and conformational mobility in homotrimeric dUTPases. <i>FEBS Letters</i> , 2004, 566, 48-54.	1.3	30
124	dUTPase and Nucleocapsid Polypeptides of the Mason-Pfizer Monkey Virus Form a Fusion Protein in the Virion with Homotrimeric Organization and Low Catalytic Efficiency. <i>Journal of Biological Chemistry</i> , 2003, 278, 38803-38812.	1.6	21
125	Catalytic and structural role of the metal ion in dUTP pyrophosphatase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5670-5675.	3.3	46
126	Altered Subunit Communication in Subfamilies of Trimeric dUTPases. <i>Biochemical and Biophysical Research Communications</i> , 2000, 279, 534-542.	1.0	42



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127	A new potent calmodulin antagonist with arylalkylamine structure: crystallographic, spectroscopic and functional studies. <i>Journal of Molecular Biology</i> , 2000, 297, 747-755.	2.0	40
128	Pyruvate Kinase as a Microtubule Destabilizing Factor in Vitro. <i>Biochemical and Biophysical Research Communications</i> , 1999, 254, 430-435.	1.0	30
129	The complete triphosphate moiety of non-hydrolyzable substrate analogues is required for a conformational shift of the flexible C-terminus in E. coli dUTP pyrophosphatase. <i>FEBS Letters</i> , 1998, 421, 83-88.	1.3	40
130	Simultaneous Binding of Drugs with Different Chemical Structures to Ca <sup>2+</sup> -Calmodulin: A Crystallographic and Spectroscopic Study. <i>Biochemistry</i> , 1998, 37, 15300-15310.	1.2	75
131	Alternative Binding of Two Sequential Glycolytic Enzymes to Microtubules. <i>Journal of Biological Chemistry</i> , 1997, 272, 25542-25546.	1.6	73
132	Characterization of Microtubule-Phosphofructokinase Complex: Specific Effects of MgATP and Vinblastine. <i>Biochemistry</i> , 1997, 36, 2051-2062.	1.2	33
133	Interaction of a new bis-indol derivative, KAR-2 with tubulin and its antimetabolic activity. <i>British Journal of Pharmacology</i> , 1997, 121, 947-954.	2.7	21
134	The interaction of a new anti-tumour drug, KAR-2 with calmodulin. <i>British Journal of Pharmacology</i> , 1997, 121, 955-962.	2.7	17
135	Crystallization and preliminary diffraction analysis of Ca <sup>2+</sup> -calmodulin-drug and apocalmodulin-drug complexes. , 1997, 28, 131-134.		5
136	Flexible glycine rich motif of Escherichia coli deoxyuridine triphosphate nucleotidohydrolase is important for functional but not for structural integrity of the enzyme. , 1997, 28, 568-579.		51
137	Flexible glycine rich motif of Escherichia coli deoxyuridine triphosphate nucleotidohydrolase is important for functional but not for structural integrity of the enzyme. , 1997, 28, 568.		1
138	Specific characteristics of phosphofructokinase-microtubule interaction. <i>FEBS Letters</i> , 1996, 379, 191-195.	1.3	25
139	Specific Derivatization of the Active Site Tyrosine in dUTPase Perturbs Ligand Binding to the Active Site. <i>Biochemical and Biophysical Research Communications</i> , 1996, 219, 294-300.	1.0	38
140	Triosephosphate Isomerase Deficiency: Predictions and Facts. <i>Journal of Theoretical Biology</i> , 1996, 182, 437-447.	0.8	26
141	Anti-calmodulin potency of indol alkaloids in in vitro systems. <i>European Journal of Pharmacology</i> , 1995, 291, 73-82.	2.7	23
142	Identification of tyrosine as a functional residue in the active site of Escherichia coli dUTPase. <i>BBA - Proteins and Proteomics</i> , 1994, 1205, 146-150.	2.1	24
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